



1/10

## FIG. 1

## SEQUENCE LISTING

5 <110> WARNER-LAMBERT  
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 <130> A0000434  
 10 <140>  
 <141>  
 <160> 1  
 15 <170> PatentIn Ver. 2.1  
 <210> 1  
 <211> 471  
 20 <212> PRT  
 <213> Homo sapiens  
 <400> 1  
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 25 1 5 10 15  
 Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser  
 20 30  
 Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His  
 30 35 40 45  
 Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met  
 50 55 60  
 35 Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr  
 65 70 75 80  
 Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys  
 40 85 90 95  
 Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys  
 100 105 110  
 45 Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp  
 115 120 125  
 Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val  
 130 135 140  
 50 Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile  
 145 150 155 160  
 Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr  
 165 170 175  
 55 Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly  
 180 185 190

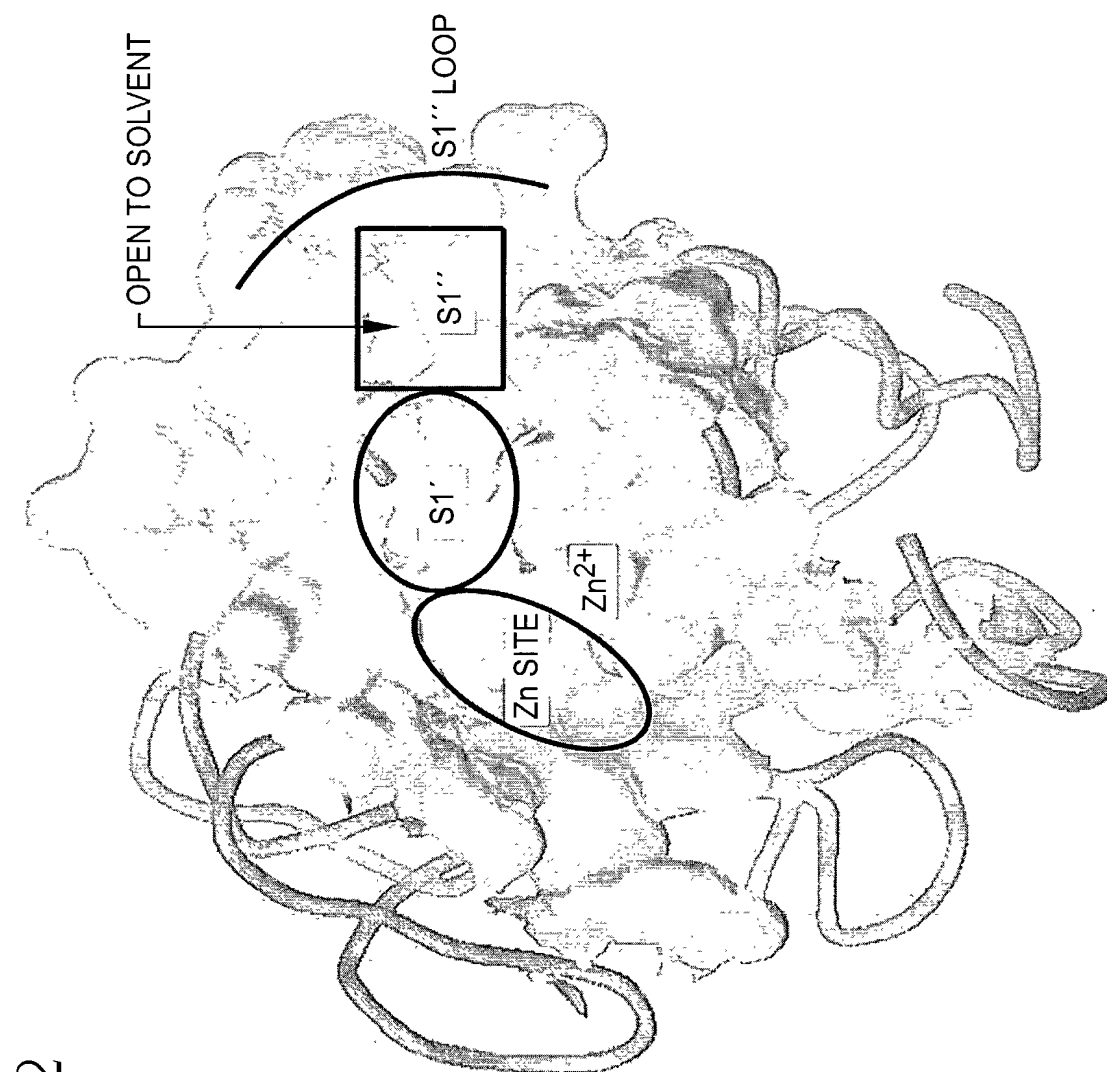
10/075,069

2/10

FIG. 1A

	Pro	Asn	Tyr	Gly	Gly	Asp	Ala	His	Phe	Asp	Asp	Asp	Glu	Thr	Trp	Thr
		195						200					205			
5	Ser	Ser	Ser	Lys	Gly	Tyr	Asn	Leu	Phe	Leu	Val	Ala	Ala	His	Glu	Phe
	210						215					220				
10	Gly	His	Ser	Leu	Gly	Leu	Asp	His	Ser	Lys	Asp	Pro	Gly	Ala	Leu	Met
	225					230					235					240
	Phe	Pro	Ile	Tyr	Thr	Tyr	Thr	Gly	Lys	Ser	His	Phe	Met	Leu	Pro	Asp
					245					250					255	
15	Asp	Asp	Val	Gln	Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Pro	Gly	Asp	Glu	Asp
				260					265					270		
20	Pro	Asn	Pro	Lys	His	Pro	Lys	Thr	Pro	Asp	Lys	Cys	Asp	Pro	Ser	Leu
			275					280					285			
	Ser	Leu	Asp	Ala	Ile	Thr	Ser	Leu	Arg	Gly	Glu	Thr	Met	Ile	Phe	Lys
	290						295					300				
25	Asp	Arg	Phe	Phe	Trp	Arg	Leu	His	Pro	Gln	Gln	Val	Asp	Ala	Glu	Leu
	305					310					315					320
	Phe	Leu	Thr	Lys	Ser	Phe	Trp	Pro	Glu	Leu	Pro	Asn	Arg	Ile	Asp	Ala
					325					330					335	
30	Ala	Tyr	Glu	His	Pro	Ser	His	Asp	Leu	Ile	Phe	Ile	Phe	Arg	Gly	Arg
				340					345					350		
35	Lys	Phe	Trp	Ala	Leu	Asn	Gly	Tyr	Asp	Ile	Leu	Glu	Gly	Tyr	Pro	Lys
			355					360					365			
	Lys	Ile	Ser	Glu	Leu	Gly	Leu	Pro	Lys	Glu	Val	Lys	Lys	Ile	Ser	Ala
	370						375					380				
40	Ala	Val	His	Phe	Glu	Asp	Thr	Gly	Lys	Thr	Leu	Leu	Phe	Ser	Gly	Asn
	385					390					395					400
	Gln	Val	Trp	Arg	Tyr	Asp	Asp	Thr	Asn	His	Ile	Met	Asp	Lys	Asp	Tyr
					405					410					415	
45	Pro	Arg	Leu	Ile	Glu	Glu	Asp	Phe	Pro	Gly	Ile	Gly	Asp	Lys	Val	Asp
				420					425					430		
50	Ala	Val	Tyr	Glu	Lys	Asn	Gly	Tyr	Ile	Tyr	Phe	Phe	Asn	Gly	Pro	Ile
			435					440					445			
	Gln	Phe	Glu	Tyr	Ser	Ile	Trp	Ser	Asn	Arg	Ile	Val	Arg	Val	Met	Pro
	450						455					460				
55	Ala	Asn	Ser	Ile	Leu	Trp	Cys									
	465					470										

10075,069



**FIG. 3** SYNTHESIS EXAMPLE 1 BINDING MODE

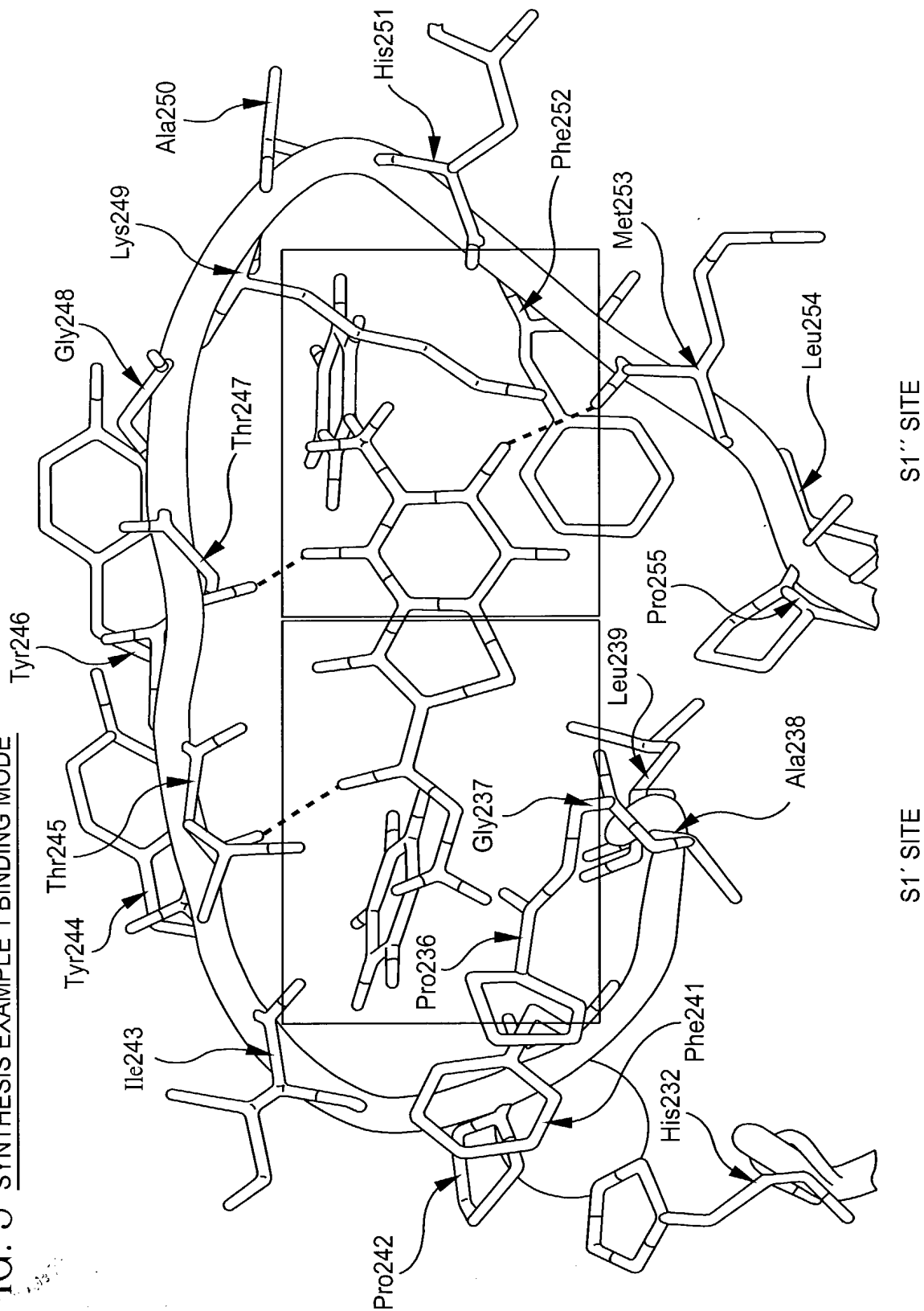
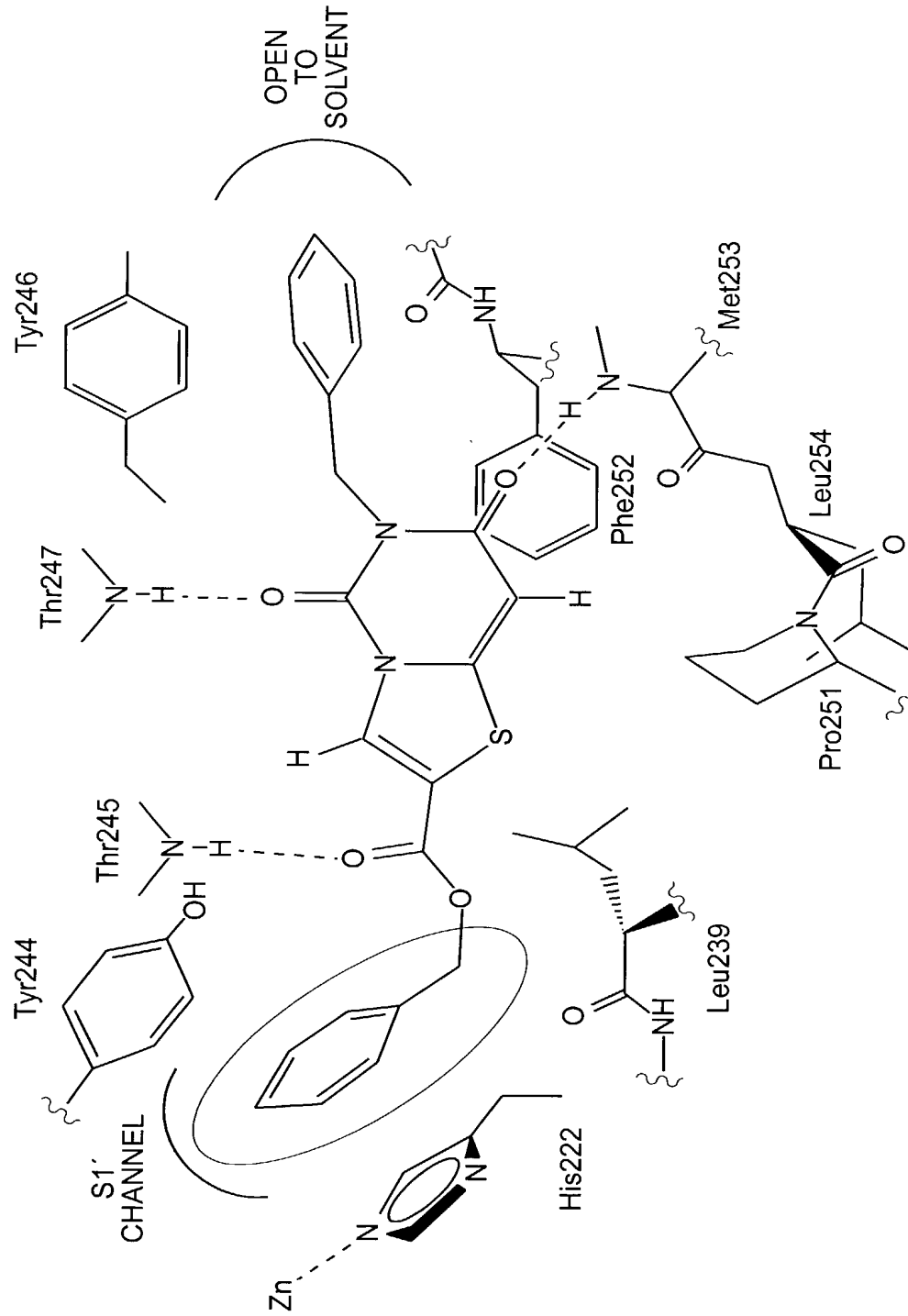
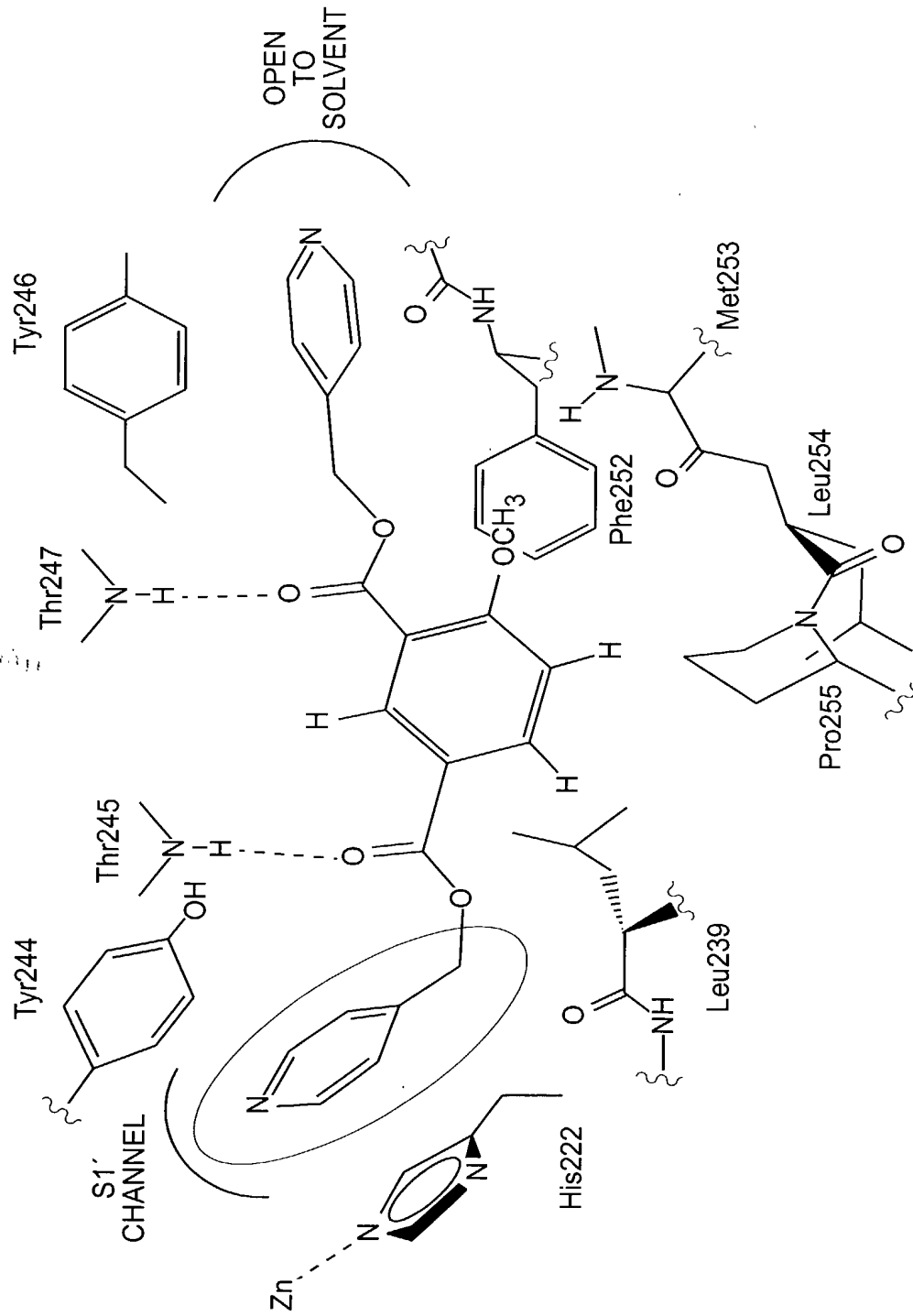


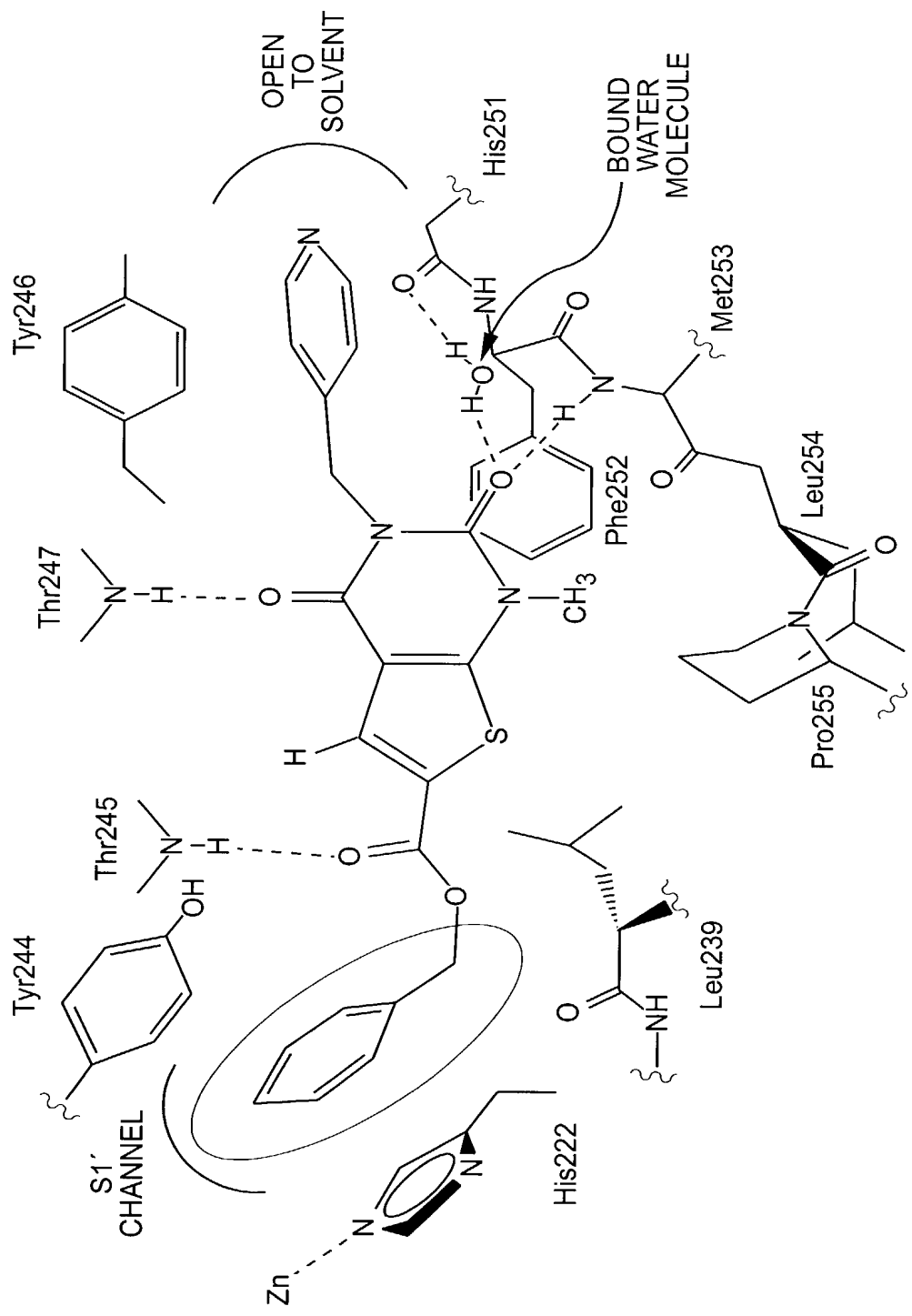
FIG. 4 SYNTHESIS EXAMPLE 1 BINDING MODE



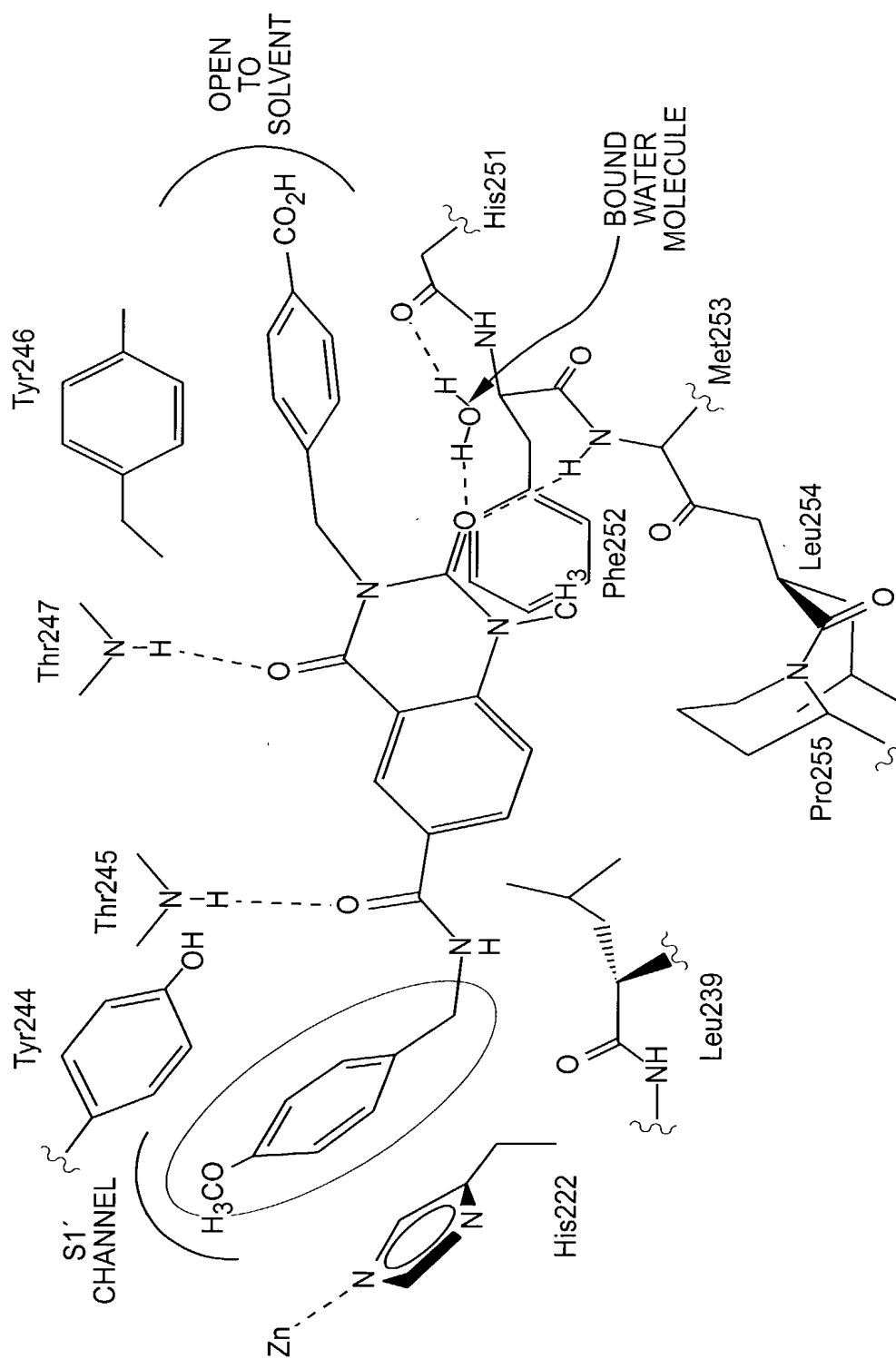
**FIG. 5** SYNTHESIS EXAMPLE 10 BINDING MODE



**FIG. 6** FUSED BICYCLIC PYRIMIDONES-BINDING MODE



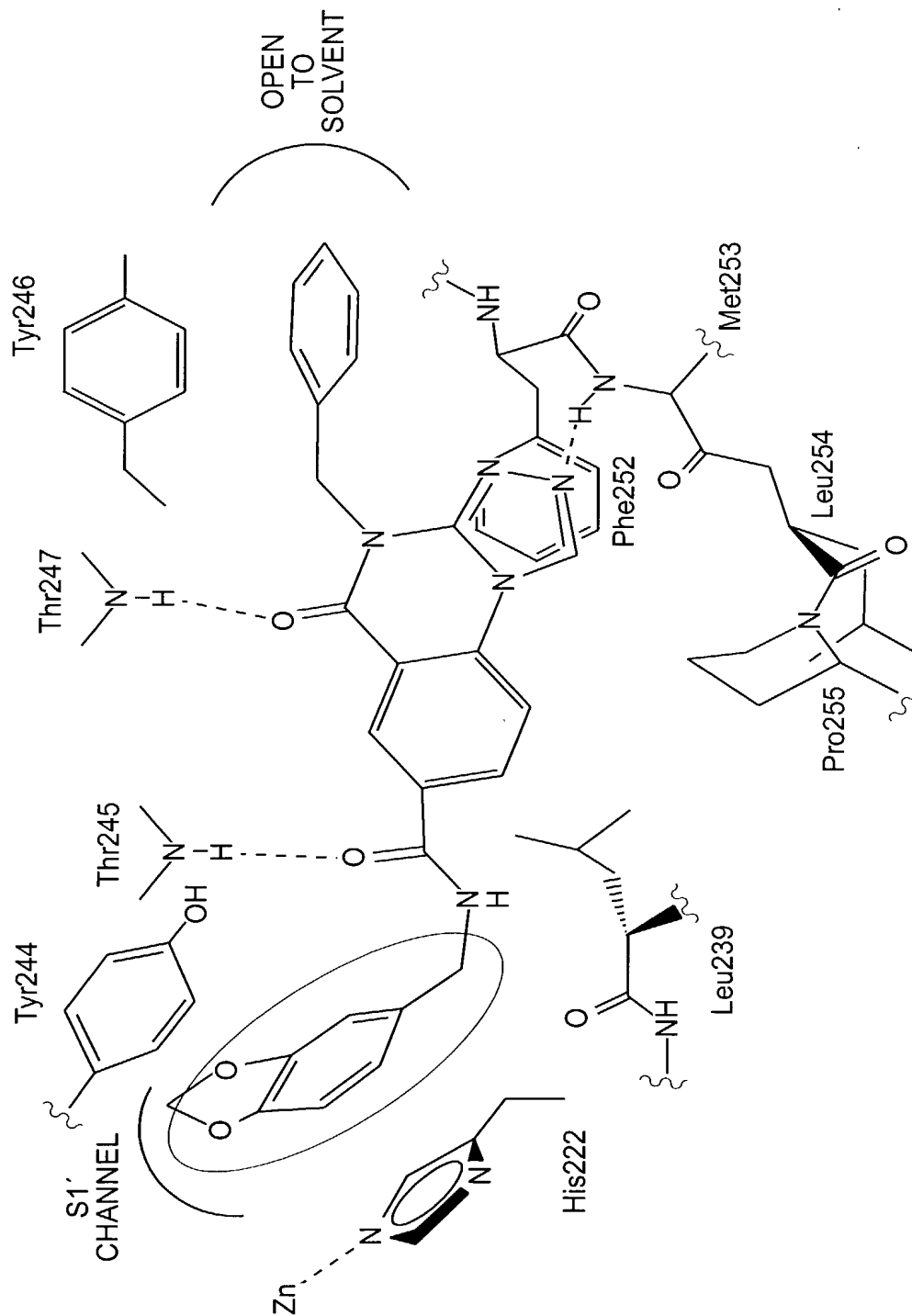
**FIG. 7** SYNTHESIS EXAMPLE 39 BINDING MODE



**10/075,069**



**FIG. 8** SYNTHESIS EXAMPLE 57 BINDING MODE



**FIG. 9** COORDONATES IN THE SPACE OF THE HYDROPHOBIC GROUPS AND HYDROGEN BOND ACCEPTORS OF THE PHARMACOPHORE

